IN THE CLAIMS

This listing of the claims replaces all prior versions of the claims in the application.

1-11. (canceled)

12. (currently amended): A method for detecting the presence of West Nile virus (WNV) in a biological sample, the method comprising:

isolating nucleic acids from a biological sample suspected of containing WNV;

amplifying the nucleic acids using a sense and an antisense primer wherein each of the primers is not more than about 60 nucleotides in length and is sufficiently complementary to a portion of the ~~sense and~~ antisense and sense strands, respectively, of the isolated nucleic acid to hybridize therewith to allow amplification of said WNV nucleic acids, and

(a) the sense primer comprises SEQ ID NO:34 ~~or a nucleotide sequence having at least 90% sequence identity thereto, or SEQ ID NO:37 or a nucleotide sequence having at least 90% sequence identity thereto, or SEQ ID NO:42 or a nucleotide sequence having at least 90% sequence identity thereto~~;

(b) the antisense primer comprises SEQ ID NO:35 ~~or a nucleotide sequence having at least 90% sequence identity thereto when the sense primer is SEQ ID NO:34, or the antisense primer comprises SEQ ID NO:38 or a nucleotide sequence having at least 90% sequence identity thereto when the sense primer is SEQ ID NO:37, or the antisense primer comprises SEQ ID NO:43 or a nucleotide sequence having at least 90% sequence identity thereto when the sense primer is SEQ ID NO:42~~; and

detecting the presence of the amplified WNV nucleic acids as an indication of the presence of WNV in the sample.

13. (original): The method of claim 12, wherein the nucleic acids are isolated from the biological sample by a method comprising:

(a) contacting a solid support comprising capture nucleic acids associated therewith with a biological sample under hybridizing conditions wherein WNV nucleic acid strands, if present in the biological sample, hybridize with the capture nucleic acids; and

(b) separating the solid support from the sample.

14. (original): The method of claim 13, wherein the solid support comprises beads.

15. (original): The method of claim 14, wherein the beads are magnetic beads.

16. (original): The method of claim 15, wherein the isolating, amplifying and detecting are performed in a single container.

17. (currently amended): The method of claim 13, wherein the capture nucleic acids comprise one or more oligonucleotides, wherein each of the oligonucleotides is not more than about 60 nucleotides in length and comprises at least 10 contiguous nucleotides from a sequence selected from the group consisting of SEQ ID NOS:~~1-16,~~ 8 and 45~~, 46 and 50~~, wherein the capture nucleic acids selectively bind to WNV nucleic acids from said biological sample.

18. (original): The method of claim 17, wherein the capture nucleic acids further comprise a homopolymer chain of about 10-25 nucleotides in length, selected from the group consisting of polyA, polyT, polyG, polyC, and polyU.

19. (original): The method of claim 18, wherein the homopolymer chain is a polyA chain.

20. (currently amended): The method of claim 12, wherein amplifying comprises RT-PCR, transcription-mediated amplification (TMA) or ~~TaqMan™~~ a fluorogenic 5' nuclease assay, or a combination thereof.

21. (currently amended): The method of claim 13, wherein amplifying comprises ~~TaqMan™~~ a fluorogenic 5' nuclease assay using the sense primer and the antisense primer and detecting is done using at least one probe comprising a detectable label.

22. (currently amended): The method of claim 21, wherein the at least one probe is not more than 60 nucleotides in length and comprises ~~(a)~~ the sequence of SEQ ID NO:52 or the sequence of SEQ ID NO:53 when the sense primer comprises the sequence of SEQ ID NO:34 ~~or (b) the sequence of SEQ ID NO:54 when the sense primer comprises the sequence of SEQ ID NO:37 or (c) the sequence of SEQ ID NO:55 when the sense primer comprises the sequence of SEQ ID NO:42~~, wherein the probe selectively binds to said WNV nucleic acids.

23. (original): The method of claim 22, wherein the method comprises using a probe comprising the sequence of SEQ ID NO:52 and a probe comprising the sequence of SEQ ID NO:53 when the sense primer comprises the sequence of SEQ ID NO:34.

24. (original): The method of either of claims 22 or 23, wherein the probe further comprises detectable labels at the 5'-end and at the 3'-end.

25. (original): The method of claim 21, wherein the detectable label is a fluorescent label selected from the group consisting of 6-carboxyfluorescein (6-FAM), tetramethyl rhodamine (TAMRA), and 2', 4', 5', 7',- tetrachloro -4-7- dichlorofluorescein (TET).

26. (original): The method of claim 12, wherein an internal control sequence is present.

27. (original): The method of claim 26, wherein the internal control sequence comprises the nucleotide sequence of Figure 2 (SEQ ID NO:17).

28. (original): The method of claim 27, further comprising a detectably labeled probe sequence for the internal control sequence.

29. (currently amended): The method of claim 28, wherein the detectably labeled probe sequence for the internal control sequence comprises the sequence of SEQ ID NO:40 ~~or SEQ ID NO:41~~.

30-40. (canceled)